The listing of claims will replace all prior versions and listings of claims in the application.

Listing of Claims:

1–98 (cancelled)

99. (currently amended)   A method of identifying a set of oligonucleotides for use in a physical recombination procedure, the method comprising:

(a) providing two or more parental character strings representing ~~one~~ two or more polynucleotides or polypeptides, which character strings, when aligned for maximum identity, comprise at least one region of heterology;

(b) aligning the parental character strings to identify one or more regions of pairwise homology;

(c) manipulating the ~~one~~ two or more parental character strings by applying a crossover operator to a point selected outside an identified pairwise homology region to thereby computationally generate one or more derivative character strings; and

(d) from the one or more derivative character strings, computationally selecting a set of character substrings having sequences that identify the set of oligonucleotides for *in vitro* recombination,

wherein the selected set of character substrings identifies at least one oligonucleotide comprising a chimeric nucleic acid sequence that comprises subsequences from at least two of the parental character strings, and

wherein the subsequences from the at least two parental character strings are separated by a crossover point.

100. (previously presented)   The method of claim 99, further comprising:

identifying one or more frame shift mutations or premature terminations among the derivative character strings; and

removing or repairing derivative character strings possessing the one or more frame shift mutations or premature terminations.

101. (previously presented)   The method of claim 99, further comprising, applying a genetic operator to the one or more parental character strings, wherein the genetic operator is selected from the group consisting of multiplication, mutation, fragmentation, and ligation.

102-104. (Cancelled)

105. (currently amended) A method of identifying a set of oligonucleotides for use in a physical recombination procedure, the method comprising:

(a) providing two or more parental character strings representing ~~one~~ two or more polynucleotides or polypeptides, which character strings, when aligned for maximum identity, comprise at least one region of heterology;

(b) aligning the parental character strings to identify one or more regions of pairwise homology;

(c) manipulating the ~~one~~ two or more parental character strings by applying a crossover operator to a point selected within an identified pairwise homology region to thereby computationally generate one or more derivative character strings; and

(d) from the one or more derivative character strings, computationally selecting a set of character substrings having sequences that identify the set of oligonucleotides for *in vitro* recombination₄[.]

wherein the selected set of character substrings identifies at least one oligonucleotide comprising a chimeric nucleic acid sequence that comprises subsequences from at least two of the parental character strings, and

wherein the subsequences from the at least two parental character strings are separated by a crossover point, ~~and~~

~~wherein the crossover point is selected from a region of identified pairwise homology~~.

106. (previously presented) The method of claim 105, further comprising:

identifying one or more frame shift mutations or premature terminations among the derivative character strings; and

removing or repairing derivative character strings possessing the one or more frame shift mutations or premature terminations.

107. (previously presented) The method of claim 105, further comprising, applying a genetic operator to the one or more parental character strings, wherein the genetic operator is selected from the group consisting of multiplication, mutation, fragmentation, and ligation.

108. (currently amended) The method of claim 105, wherein the at least one oligonucleotide comprising a chimeric nucleic acid sequence is at least about 10 nucleotides in length.

109. (previously presented) The method of claim 105, further comprising analyzing the one or more derivative character strings with an energy expression.

3

110. (currently amended) The method of claim 99, wherein the at least one oligonucleotide comprising a chimeric nucleic acid sequence is at least about 10 nucleotides in length.

111. (previously presented) The method of claim 99, further comprising analyzing the one or more derivative character strings with an energy expression.

112. (currently amended) A method of identifying a set of oligonucleotides for use in a physical recombination procedure, the method comprising:

(a) providing two or more parental character strings representing ~~one~~ two or more polynucleotides or polypeptides, which character strings, when aligned for maximum identity, comprise at least one region of heterology;

~~(c)~~ (b) manipulating the ~~one~~ two or more parental character strings by applying a crossover operator to computationally generate one or more derivative character strings; and

~~(d)~~ (c) from the one or more derivative character strings, computationally selecting a set of character substrings having sequences that identify the set of oligonucleotides for *in vitro* recombination,[.]

wherein the selected set of character substrings identifies at least one oligonucleotide comprising a chimeric nucleic acid sequence that comprises subsequences from at least two of the parental character strings, and

wherein the subsequences from the at least two parental character strings are separated by a crossover point.

4